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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            earched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5:
6::
7::
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112::
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Gapop 10.0 , Gapext 0.5
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461.889 Million cell updates/sec
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    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_human: *
    175
217
842
1193
938
1998
1998
2233
327
2233
595
775
1299
1299
314
485
      10
6
6
10
10
10
10
11
11
  0974WB
097561
098756
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0991XB
0971XB
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094711
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Q8r4w8 mus musculu
Q97d6f clostridium
Q8r056 mus musculu
Q9y1x8 ephydatia f
Q8rwv7 arabidopsis
Q9str8 arabidopsis
Q9str8 arabidopsis
Q97491 ovis aries
Q94711 paramecium
Q94711 paramecium
Q94711 paramecium
Q94711 paramecium
Q94714 paramecium
Q9471
                                                                                                                                                                                                                                                                                                                                                                Description
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Q9zqr4 arabidopsis	Q9ZQR4	10	408	7.5	•	
Q22095 caenorhabdi	Q22095	ហ	375	•	72.5	
O.	085853	N	243	٠	٠	
	Q9LMP0	10	733	7.6	73	
	Q9ZWD7		679		73	
	OMMIRO 0	17	462		73	
	Q99UY7		304	٠	73	
	Q40096		853	7.6	73.5	
Q8t259 dictyosteli	Q8T259	v	634	7.6	73.5	
Q97rg2 streptococc	Q97RG2	16	307	.7.6	73.5	
Q91000 gallus gall	Q91000	13	789	7.7	74	
Q9rhu5 streptomyce	Q9RHU5	N	377	7.7	74	
Q22378 caenorhabdi	Q22378	υī	966	7.7	74.5	
Q9ykv7 human immun	Q9YKV7	15	853	7.7	74.5	
Q9bi07 entamoeba h	Q9BI07	v	718	7.8		
	Q8T206	տ	706	7.8		
85	Q97E85	16	450	7.8	75	
Ω	Q8T1T4	υ	454	7.8	75.5	
Q63661 rattus norv	Q63661		1805	7.9	76	
O42637 neurospora	042637		748	7.9	76	
	045251		1404		76.5	
Q9fje3 arabidopsis	Q9FJE3	10	656		76.5	
	Q9XV87	տ	357	7.9	76.5	
	ONOX60	16	539		77	
ω	Q9M3B3	10	522		77	
O04623 arabidopsis	004623	10	968	8.0	77.5	
7	Q9YKU7	15	853		77.5	
O81819 arabidopsis	081819	10	738		77.5	
Q91mn6 arabidopsis	Q9LMN6	10	738	8.0	77.5	

ALIGNMENTS

8 8	ᅡ	Ş	Db	Ş	Qu Ma	SQ	ב קל	RI	RT	RA	ŖΡ	RN	õ	88	3	လ္လ	DE	ď	Þ	ď	AC	ID Q	KESCLI
112 BIILPRGLEYTVBECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161	81 GLILALTLYGLYSLYSWRWRQQLRTASPDTSEGYQQESLENVFYPSSET 129	57 WTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111	21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80	7 OCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAIL 56	Query Match 12.1%; Score 116.5; DB 11; Length 175; Best Local Similarity 29.4%; Pred. No. 0.0002; Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps	SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;	EMBL: AF350257: AAL83914.1:	(FFB-2001) to the	"Identification of novel TRAF3 binding protein, T3BP, which increases	Mizuno K., Irie S., Sato TA.;	SEQUENCE FROM N.A.	(2) T		Rodentia, Sciurognathi, Muridae,	Rukaryota: Metazoa: Chordata: Craniata: Vertebrata: Ruteleostomi:	Mus musculus (Mouse).	ng protein.	(TrEMBLrel. 21, Last		01-JUN-2002 (TremBirel. 21, Created)	Q8R4W8;	W6 Q8R4W8 PRELIMINARY; PRT; 175 AA.	H .

RESULT 2

Best Local Similarity

22.7%;

1.9;

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QBROSG
ID QBRO
AC QBRO
AC QBRO
DT 01-J
DT 01-J
DT 01-J
DT 01-J
DT 01-J
CO Mumm
OX NCB:
RN (1)
RN (1)
RR SEQI
RC SING
RA SEX:
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Best Local Similarity
Matches 55; Conserv
  Query Match
                                       EMBL, BC02828
Hypothetical
SEQUENCE 84
                                                                                                                                                                                                                                                                                                                                                                                     Q8R056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the
EMBL<sub>N,</sub> BC028286; AAH28286.1;
                                                                                                                                                                                                                                                                              Hypothetical 94.5 kDa protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                          01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001
01-OCT-2001
                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 824 /
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000515; BPD_transp.
                                                                                                                                                    SSUE=EYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVTPYLFAGIFYLILTTIFTGIFSK-----IEKKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFPLPAMEEGA -- TILVTTKTNDYCKSLPAALSATEIEKSIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLHACIPCQLRCSSNTPPLTCQRYCNASV----TNSVKGTNAI----LWTCLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGLTYGQTMKRITLPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TGDEIILPRGLEYTVEEC-----TCEDCI-KSKPKVDSDH
                                          al protein.
842 AA; 5
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                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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F
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                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23743 MW; 36738BCDC0DE8A2F CRC64;
                                          94478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%;
  9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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Last sequence update)
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                                                                                                        EMBL/GenBank/DDBJ
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5; Mismatches
  Score
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Pred. No. 0
                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                          734C10D715E5BC92
86.5;
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                                                                                                                                                                                                                                                                                                                                                                                                           842
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                                                                                                        databases
                                            CRC64
Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLLGMANIDLEKSR
842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217;
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                                                                                                                                                                                                                                      Mus
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RESULT 4
Q9Y1X8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y1X8
Q9Y1X8;
01-NOV-1999
                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                               ProDom; PD000001; Euk pkir
SMART; SM00261; FU; 6.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                  Suga H., Katoh K., Miyata 1.; "Sponge homologs of vertebrate protein tyrosine kinases and domain shufflings in the early evolution of animals before t
SEQUENCE
                                                                                                            Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_doma
PRINTS; PR00109; TYRKINASE
                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=99246375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Porifera;
Haplosclerida; Spongillidae; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein tyrosine EFPTK178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
           Kinase
                                                                                                                                              InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                    the parazoan-eumetazoan split demonstrated tyrosine kinases from sponge and hydra.";
                                                                                                                                                                                                                                                                                                                                                                                      Miyata T.
                                                                                                                                                                                                                                                                                                                                                                                                   Suga H.,
                                                                                                                                                                                                                             HSSP; P08631;
                                                                                                                                                                                                                                      EMBL; AB006570;
                                                                                                                                                                                                                                                  Gene 280:195-201(2001
                                                                                                                                                                                                                                                              parazoan-eumetazoan split.
                                                                                                                                                                                                                                                                                                         MEDLINE=21601119; PubMed=11738833;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=31330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydatia fluviatilis.
                                                                                                                                                                               InterPro;
                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                                 nterPro;
                                                                                                                                                                                                                                                                                                                                                                          Extensive gene duplication
                                                                                                                                                                                                                                                                                                                                           Mol. Evol.
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                  PS00107; PROTEIN KINASE ATP; 1.
PS50011; PROTEIN KINASE DOM; 1.
PS00109; PROTEIN KINASE TYR; 1.
PS00652; TMFR_NGFR_1; UNKNOWN_1.
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                                                                                                                                                                    IPR002290; Ser_thr_pkinase.
IPR001368; TNFR_c6.
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AA:
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128169 MW;
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Q9STR8;
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Hypothetical
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Q8RWV7;
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     T24C20_80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 93
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37; Conserv
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                                                                                                                                                                                                                                EEGATI 155
                                                                                                                                                                                                                                                                 SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--
                                                                                                                                                                                                                                                                                                 GLIGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP----KVDSDHCFPLPAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIVFGSIVVIFLATSIVLILFIVYRRYEHKVFKNRTQSTA---MCYSN---
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Last annotation updat
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Pred. No. 4.5;
18; Mismatches
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8; Mismatches
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Pred. No. 3.
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Best Local S
Matches 37
Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR c6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

SMO21TE; PS50017; DEATH DOWAIN; 1

PROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS00550; TNFR NGFR 2; 2.

SEQUENCE 327 AA; 36928 MW; 5 50
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TISSUE=LYMPHOCYTE;
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01-JUN-2001
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SMART; SM00312; PX; 1
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                                                                                                                                  InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6
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InterPro; IPR001683; PX. |
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1.
2.
5CFEE844B2BE387A CRC64;
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Takagi M., Takahashi H., Kabeya H., Ohashi K., "Cloning of sheep fas antigen!";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ EMBL, AB011671; BAA37093.1; -
HSSP; P25445; IDDF.
                                                                                                                                                                                                              Ovis aries (Sheep).

Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
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Choisne N., Robert C., Brottier P., Wincker P., Cattolic Choisne N., Robert M., Weissenbach J., Mewes H.W., I Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., I Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 1998 AA; 223513 MW; 8B3D6A03CD248F55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS
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                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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Pred. No. 11
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                                                                                                             Sugimoto C.,
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3 H.W., Rudd :
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                                                                                                                                                                                                                                                                                 Bovoidea;
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                                                                                                                  Onuma
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RESULT
Q94711
ID Q9
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Q8VEV6;
Q1-MAR-2002 (TrEMBLrel. 20, Cre
01-MAR-2002 (TrEMBLrel. 21, Lag
01-JUN-2002 (TrEMBLrel. 21, Lag
Olfactory receptor MOR202-36.
                                            Q94711;
Q94711;
Q1-FEB-1997
01-FEB-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                              51C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AY073792; AAL61455.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOW
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang X., Firestein S.J.;
"The olfactory receptor gene Nat. Neurosci. 0:0-0(2002).
      Paramecium
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                              surface
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97 (TrEMBLrel.
01 (TrEMBLrel.
ce protein.
m tetraurelia.
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Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 81.5;
Pred. No. 2.
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RESULT 10
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Apx hydroxyl.
InterPro; IPR000152; Apx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF-Ca.
Pfam; PF00069; pkinase; I.

ProDom; PD000001; Euk pkinase; 1.

SMART; SM000179; EGF CA; 1.

SMART; SM00001; EGF Like; 1.

SMART; SM00001; EGF Like; 1.

PROSITE; PS01186; EGF CA; UNKNOWN 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q39191, PRELIMINARY;
Q39191, 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nielsen E., You Y., Forney J.;
"Cysteine residue periodicity is a conserved structural feature variable surface proteins from Paramecium tetraurelia.";
J. Mol. Biol. 222:835-841(1991).
EMBL; M65164; AAA61740.1;
InterPro; IPR002895; Paramecium SA.
Pfam; PF01508; Paramecium SA; 25.
SEQUENCE 2233 AA; 237078 MW; C064FE0AF7BB873B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An Arabidopsis serine threonine kinase homologue with selected in yeast for its specificity for a thylakoid m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine threonine kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=93066369; PubMed=1438303;
                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001881;
nterPro; IPR000719;
                                                                                                                                                                                                                                                                                                              nterPro; IPR002290; Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d. Sci. U.S.A. 89:10989-10992(1992)
BELONGS TO THE SER/THR FAMILY OF P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-
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25.1%;
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                                                                                                                                                                                                                                                                                                        thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %; Score 81.5; Di
%; Pred. No. 20;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
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                                          Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----D
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SEQUENCE

Matches

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Matches 40
                                                                                                                                                                                                                                                                       Waterston R.;
Waterston R.;
Submitted (JUN-1999) to the EMBL/GenBan)
EMBL; AF003385; AAB54249.1; -.
EMBL; BOS164; ICXP.
HSSP; POS164; ICXP.
InterPro; IPR002007; Anim_peroxidase.
Pfam; PF03098; An_peroxidase; 1.
Pfam; PF03098; An_peroxidase; 1.
SEQUENCE 773 AA; 83992 MW; 4E3373FD
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode investigating biology. The C. elections 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=99069613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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01-JUL-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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itted (MAY-1997)
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                                                                                                                                                                                                                                 Similarity
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   SSINCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRAINGQSGFGVRTQ
                                  EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA----TE
                                                                       IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG
                                                                                                        IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV
                                                                                                                                           PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
                                                                                                                                                                            PCQLRCSSNTPPLTCQ-----RYCN----ASVTNSVKGTNAILWTCL---GLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLSGPSNVDVKIFTEDGMKKATNGYAESRILGQGGQGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
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7) to the
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                                                                                                                                                                                                              8.4%; Score 81; DB
21.7%; Pred. No. 6.6;
tive 25; Mismatches
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04,
21,
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Caenorhabditis.
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cosmid R08F11.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 81; DB
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans
                                                                                                                                                                                                                                                                                  4E3373FDA4EC67C7 CRC64;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall-associated kinase 1 (Putative wall-associated WAKI OR F16F4.6.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae. Strontonio.
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081820;
                                                                                                                                                                                                         PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; EGF 2; UNKNOWN 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Serine/threonine-protein kinase; Transferase.

SEQUENCE 735 AA; 81211 MW; AAD41A28296093E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Z.H., Cheeseman I., He D., Kohorn B.D., 
"A cluster of five cell wall associated receptor k 
are expressed in specific organs of Arabidopsis."; 
Plant Mol. Biol. 39:1189-1196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF Ca. d
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY039917; AAK64021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ009696; CAA08794.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99308512; PubMed=10380805;
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase;
ProDom; PD000001; Euk p
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290;
InterPro; IPR004040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY
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                                    46
                                                                                                                                                                                                                                                                                                                                                    SM00221; STYKc;
                                                                                                        8
                                                                                                                                           Similarity
39; Conser
TMSCKRKEFAWTTILLTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ 382
                                                                     CRCNEGFDGNPYLSAGCQDVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT
                                  TNSVK----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                                                      CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR-----YCNA----SV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDON
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                                                                                                                                           Conservative
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                                                                                                                                                         8.3%;
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STY_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                         pkinasė; 1.
                                                                                                                                           27;
                                                                                                                                                         Score 80;
Pred. No.
                                                                                                                                           Mismatches
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OF PROTEIN
                                                                                                                                           Indels
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Minx P.

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GMANID-----LEKSRTG--DEILPRGLEYTV 123

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Q8VFW0
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Q26489
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Best Local S
Matches 39
                                                            QBVFW0;

01-MAR-2002 (TrEMBLrel. 20, Cr.

01-MAR-2002 (TrEMBLrel. 20, La.

01-JUN-2002 (TrEMBLrel. 21, La.

Olfactory receptor MOR202-16.

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                        Protease.
SEQUENCE
                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase S8; 1.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD00717; P domain; 1.
SMART; SM00261; FU; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=7108;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z68888; CAA93116.1; --
HSSP; Q99405; IMPT.
InterPro; IPR002174; Furin-like.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
                                                                                                                                            Q8VFW0
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PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and functional characterization of FURIN from frugiperda (Sf9) cells."; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH
                                                                                                                                                                                                                                                             GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG-----
                                                                                                                                                                                                                                                                                       TCLGLS-----LIISLAV-----FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN
                                                                                                                                                                                                                                                                                                                                          CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W
                                                                                                                                                                                                                                                                                                                 CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSGAGPSNVDVKIFTEDGMKKATNGYAESRILGQGGQGTV 423
                                                                                                                                                                                                            --VEYSR-----LPRTDVDFTV----LTSCTDQEGPVEYEH 1289
                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                        1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                            PRELIMINARY;
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                                    Chordata;
Rodentia;
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20, Last sequence up
21, Last annotation
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; Pred. No. 17;
26; Mismatches
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                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 15
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Search completed: June 23, Job time: 85.0818 secs
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Best Local S
Matches 35
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Best Local (
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SEQUENCE
                                                                                                                                                                                                                                                                                 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Stanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKOG6184; BAB15387.1;
SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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01-MAR-2001
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PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/C
EMBL; A7073405; AAL61068.1; -
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
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"The olfactory receptor gene superfamily Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                              l Similarity
35; Conserv
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                                                         IMGVYTLLTTHLN
                                                                                   -EGATILVTTKTN 162
                                                                                                               PNLDLNLDR----DLVLP-DVSYQVESSEEDQSQTMDPQGQTLLLFLFVDFHSAFPVQQME
                                                                                                                                          ANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPK---
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llarity 26.3%;
Conservative 1
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llarity 30.4%;
Conservative 1
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                2003, 08:39:06
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Pred. No. 4.4;
15; Mismatches
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Pred. No. 7.2;
L7; Mismatches
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                                                                                                                                                                                                                                                       DB 4;
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Shibahara
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